

**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/842,827**

TEAM 8

DATE: 09/11/97
TIME: 11:39:07

INPUT SET: S20239.raw

1800

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

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SEP 25 1997

GROUP 1800

SEQUENCE LISTING

1
2 (1) General Information:
3
4 (i) APPLICANT: LEUNG, David W.
5 TOMPKINS, Christopher K.
6
7 (ii) TITLE OF INVENTION: HUMAN PHOSPHATIDIC ACID PHOSPHATASE
8
9 (iii) NUMBER OF SEQUENCES: 21
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: Foley & Lardner
13 (B) STREET: 3000 K Street, N.W., Suite 500
14 (C) CITY: Washington
15 (D) STATE: D.C.
16 (E) COUNTRY: USA
17 (F) ZIP: 20007-5109
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Floppy disk
21 (B) COMPUTER: IBM PC compatible
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER: US 08/842,827
27 (B) FILING DATE: 17-APR-1997
28 (C) CLASSIFICATION:
29
30 (viii) ATTORNEY/AGENT INFORMATION:
31 (A) NAME: BENT, Stephen A.
32 (B) REGISTRATION NUMBER: 29,768
33 (C) REFERENCE/DOCKET NUMBER: 77319/125
34
35 (ix) TELECOMMUNICATION INFORMATION:
36 (A) TELEPHONE: (202)672-5300
37 (B) TELEFAX: (202)672-5399
38 (C) TELEX: 904136
39
40
41 (2) INFORMATION FOR SEQ ID NO:1:
42
43 (i) SEQUENCE CHARACTERISTICS:
44 (A) LENGTH: 1563 base pairs
45 (B) TYPE: nucleic acid
46

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PATENT APPLICATION US/08/842,827DATE: 09/11/97
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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: linear
49
50
51
52 (ix) FEATURE:
53 (A) NAME/KEY: CDS
54 (B) LOCATION: 342..1193
55

56 (ix) FEATURE:
57 (A) NAME/KEY: mat_peptide
58 (B) LOCATION: 342..1193
59
60

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62

63	CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT	60
64	GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCACTAACC	120
65	GAGTGTTCGC GGGGGCTGTG AGGGGAGGGC CCCGGGCGCC ATTGCTGGCG GTGGGAGCGC	180
66	CGCCCGGTCT CAGCCCCCCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC	240
67	GGGGCCGTCTG CCAGCCCCGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCCCGCA	300
68	CCTCATTCCA TCGCCCTTGC CGGGCAGCCC GGGCAGAGAC C ATG TTT GAC AAG	353
69	Met Phe Asp Lys	
70	1	
71	ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT	401
72	Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala	
73	5 10 15 20	
74	GGATTG CCT TTT GCA ATT CTT ACT TCA AGG CAT ACC CCC TTC CAA CGA	449
75	Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg	
76	25 30 35	
77	GGA GTA TTC TGT AAT GAT GAG TCC ATC AAG TAC CCT TAC AAA GAA GAC	497
78	Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro Tyr Lys Glu Asp	
79	40 45 50	
80	ACC ATA CCT TAT GCG TTA TTA GGT GGA ATA ATC ATT CCA TTC AGT ATT	545
81	Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile Pro Phe Ser Ile	
82	55 60 65	
83	ATC GTT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC TGT AAC CTT TTG	593
84	Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn Leu Leu	
85	70 75 80	
86	CAC TCA AAT TCC TTT ATC AGG AAT AAC TAC ATA GCC ACT ATT TAC AAA	641
87	His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile Tyr Lys	
88	85 90 95 100	

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153 ACATAGTTAC CTTTAACCTCA GTGGTTATCT AATAGCTCTA AACTCATCAA AAAAACCTCCA 1403
154
155 AGCCTTCCAC CAAAACAGTG CCCCCACCTGT ATACATTCTT ATTAAAAAAA TGTAAATGCTT 1463
156
157 ATGTATAAAC ATGTATGTAA TATGCTTTCT ATGAATGATG TTTGATTAA ATATAATACA 1523
158
159 TATTAAAATG TATGGGAGAA CCAAAAAAAA AAAAAAAA 1563
160
161
162 (2) INFORMATION FOR SEQ ID NO:2:
163
164 (i) SEQUENCE CHARACTERISTICS:
165 (A) LENGTH: 284 amino acids
166 (B) TYPE: amino acid
167 (D) TOPOLOGY: linear
168
169 (ii) MOLECULE TYPE: protein
170
171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
172
173 Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys
174 1 5 10 15
175
176 Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr
177 20 25 30
178
179 Pro Phe Gln Arg Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro
180 35 40 45
181
182 Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile
183 50 55 60
184
185 Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr
186 65 70 75 80
187
188 Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala
189 85 90 95
190
191 Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser
192 100 105 110
193
194 Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro
195 115 120 125
196
197 His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser
198 130 135 140
199
200 Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val
201 145 150 155 160
202
203 Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met
204 165 170 175
205
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206 Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly
207 180 185 190
208
209 Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala
210 195 200 205
211
212 Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His
213 210 215 220
214
215 Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile
216 225 230 235 240
217
218 Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe
219 245 250 255
220
221 Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro
222 260 265 270
223
224 Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
225 275 280
226
227 (2) INFORMATION FOR SEQ ID NO:3:
228
229 (i) SEQUENCE CHARACTERISTICS:
230 (A) LENGTH: 1566 base pairs
231 (B) TYPE: nucleic acid
232 (C) STRANDEDNESS: single
233 (D) TOPOLOGY: linear
234
235
236
237 (ix) FEATURE:
238 (A) NAME/KEY: CDS
239 (B) LOCATION: 342..1196
240
241 (ix) FEATURE:
242 (A) NAME/KEY: mat_peptide
243 (B) LOCATION: 342..1196
244
245
246 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
247
248 CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT 60
249
250 GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCACTAAC 120
251
252 GAGTGTTCGC GGGGGCTGTG AGGGGAGGGC CCCGGGCGCC ATTGCTGGCG GTGGGAGCGC 180
253
254 CGCCCCGGTCT CAGCCCCCCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC 240
255
256 GGGGCCGTCTG CCAGCCCCGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCCCGCA 300
257
258 CCTCATTCCA TCGCCCTTGC CGGGCAGGCC GGGCAGAGAC C ATG TTT GAC AAG 353

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SEQUENCE VERIFICATION REPORT
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